

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: December 6, 2002, 22:41:46 ; Search time 2691.5 Seconds
(without alignments)
16489.608 Million cell updates/sec
Title: US-10-025-514-7
Perfect score: 1525
Sequence: 1 tctagaccatgctggaag.....ccaaactcagaagtatgac 1525

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl :

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sy.*
- 12: gb_un.*
- 13: gb_vl.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	630.4	41.3	1308	6	AR111412	AR111412 Sequence
2	629.4	41.3	1185	6	AR111411	AR111411 Sequence
3	442.4	29.0	1345	9	HUMALATB	M11465 Human alpha
4	438	28.7	1434	6	E00631	E00631 DNA encodin
5	436.4	28.6	1312	6	I02706	I02706 Sequence 1
6	434.8	28.5	1584	9	BC011991	BC011991 Homo sapi
7	433.2	28.4	1352	6	AX335339	AX335339 Sequence
8	433.2	28.4	1352	6	HUMALATM	K01396 Human alpha
9	433.2	28.4	1371	6	AX335338	AX335338 Sequence
10	433.2	28.4	1371	9	HSATPR1	X01683 Human mRNA
11	433.2	28.4	1399	9	AK026174	AK026174 Homo sapi
12	433.2	28.4	1434	6	E00195	E00195 cDNA encodi
13	433.2	28.4	1434	6	I04196	I04196 Sequence 3
14	433.2	28.4	1434	6	I04272	I04272 Sequence 1
15	433.2	28.4	1434	6	I07849	I07849 Sequence 2
16	433.2	28.4	1435	6	AX019486	AX019486 Sequence
17	433.2	28.4	2478	17	AF130088	AF130088 Homo sapi
18	431.6	28.3	1337	9	HUMALAT2	J02619 Human 2 typ
19	431.6	28.3	1378	6	I02398	I02398 Sequence 8
20	431.6	28.3	1431	9	BC015642	BC015642 Homo sapi
21	431.6	28.3	2571	17	AF113676	AF113676 Homo sapi
22	430.4	28.2	1185	6	AR111410	AR111410 Sequence
23	430	28.2	1293	6	I07949	I07949 Sequence 2
24	430	28.2	1317	6	I00556	I00556 Sequence 2
25	430	28.2	1378	6	I03509	I03509 Sequence 6
26	430	28.2	1378	6	I07947	I07947 Sequence 4
27	430	28.2	1434	6	I01352	I01352 Sequence 1
28	428.4	28.1	1308	9	BABALATA	J00321 Papio hamad
29	428.4	28.1	1378	6	I01227	I01227 Sequence 2
30	426.8	28.0	1185	6	A01846	A01846 Human mRNA
31	418.4	27.4	1191	9	AB004044	AB004044 Cercopith
32	411.2	27.0	1390	6	AX202089	AX202089 Sequence
33	408.8	26.8	1356	6	I36163	I36163 Sequence 16
34	407.2	26.7	1356	6	I36161	I36161 Sequence 12
35	404	26.5	1356	6	I36164	I36164 Sequence 18
36	401.4	26.3	2013	6	AX472008	AX472008 Sequence
37	392.2	25.7	1351	10	AB000550	AB000550 Spermophi
38	389	25.5	1372	10	AB000552	AB000552 Callosciu
39	386.8	25.4	1351	4	SSANTIELA	X88780 S.scrofa mr
40	378	24.8	1306	10	RATATRA1	M32247 Rat alpha-1
41	377.4	24.7	1352	10	S77822	S77822 alpha-i-ant
42	376.4	24.7	1380	10	RATAP1	D00675 Rat mRNA fo
43	376	24.7	1343	10	AB000546	AB000546 Tamias si
44	375.6	24.6	1242	6	E13268	E13268 Tamias asia
45	370.6	24.3	1380	4	BTA1AT	X63129 B.taurus mr

ALIGNMENTS

RESULT 1	AR111412	AR111412	1308 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	Sequence 6 from patent US 6127145.					
DEFINITION	AR111412					
ACCESSION	AR111412					
VERSION	AR111412.1	GI:12828260				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1308)					
AUTHORS	Sutcliffe, D. and Rodriguez, R.L.					
TITLE	Production of .alpha..sub.1 -antitrypsin in plants					
JOURNAL	Patent: US 6127145-A 6 03-OCT-2000;					
FEATURES	Location/Qualifiers					

Db	501	ATAAGTTTTTGGAGGATGTTAAAGCTGTACCACTCAGAAGCCYTCAGTCAACTTCG	560
Qy	778	GTGATACTGAGGAGCTAAAAACCAAAATAAGTANTGTTTCAGAAAGCCACCCAGGTA	837
Db	561	GGGACACGAGAGGCCAAGAACAGATCAACGATATACGTGGAGAAGGTTACTCAAGGGA	620
Qy	838	AGATCGTTGACCTAGTTAAAGRAATTAGATCGTGATACCGCTCTTCGCACTAGTTAACTATA	897
Db	621	AAATTTGGGATTTGGTCAAGGAGCTTGACAGAGACACAGTTTTTGTCTGTGTGAATTACA	680
Qy	898	TTTTTTCAAGGGTAAGTGGGAACGTCCTTTTCGAGGTTAAAGATACTAGAAGGAAGATT	957
Db	681	TCCTCTTTAAAGGCAATGGGAGAGACCCCTTTTGAAGTCAAGGACACCCGAGGAAGGACT	740
Qy	958	TTCATGTTGATCAAGTTACTACTGTCAAAAGTTCCTCAATGATGAAGAAGACTGGGTATGTCA	1017
Db	741	TCCACGTGGACAGGTGACACCGTGAAGGTGCCCTATGATGAAGCGTTTAGGCATGTTTA	800
Qy	1018	ATATTCAACATTCGAAAAAATTAAGTTCTTGGTCTTATTAATGAAGTATTTAGGTAAAG	1077
Db	801	ACATCCAGCACTGTAAGAAAGCTGTCGAGCTGGTGCTCTGATGAAATACCTGGGCAATG	860
Qy	1078	CTACTGCTATTTTTTTTTTACCAGAGGAAGGTAAAGCTTCAACATTTAGAGAATGAGTTGA	1137
Db	861	CCACCGCATCTTCTTCTCGCTGATGAGGGGAAACTACAGCACTGGAAAAATCAACTCA	920
Qy	1138	CTCATGACATATTACTAAATTTTTAGAGAAGGATCGTGAGCGCTTCCTGCAACC	1197
Db	921	CCNCGATATCATCACCAAGTTCTCGGAAATGAAGACAGAAGGCTGCCAGCTTACATT	980
Qy	1198	TGCCAAAGTTAAAGTATCACCGGTACTTACGACTTAAAATCTGTTTTAGGCCAGTTAGSTA	1257
Db	981	TACCCAACTGTCCATTACTGNAACCTATGATCTGAAGAGCGTCTGGGTCACTGGGCA	1040
Qy	1258	TTACCAAAGTTTTTCTTAACGGTGGCCGATTTGAGTGGTGTACTGAAGAAGCTCCATTA	1317
Db	1041	TCACTAAGGTCTTCAGCAATGGGGTGACCTCTCCGGGGTCACAGAGGAGGCCACCCCTGA	1100
Qy	1318	AATGAGTAAAGCTGTTTCAAAAGCCGTCTTAACHTATTTGATGAAGAGGTACCGAGGCCG	1377
Db	1101	AGCTCTCAAAGGCCGTGCATAAGGCTGTGCTGACCATCGAGGAAAGGGACTGAAGCTG	1160
Qy	1378	CCGGCGTATGTTCCCTGGAGCTATTCCAATGAGCATTCACACAGAAGTTAAATTTAATA	1437
Db	1161	CTGGGGCATGTTTTTTAGAGGCCATACCCATGCTATCCCCCGAGGTCAAGTTCAACA	1220
Qy	1438	AACCATTCGTTTTTCTTGATGTCGAGCAGACACTTAAAGGCCATTTGTTTATGGGTAAAG	1497
Db	1221	AACCCCTTTGTCTTCTTAATGATTGAACAAATACCAGTCTCCCTCTGTCATGGGAAAG	1280
Qy	1498	TTGTCAAACCACTCAGAAGTA	1519
Db	1281	TGGTGAATCCCAACCCAAAAATA	1302

RESULT 5	
I02706	
LOCUS	I02706
DEFINITION	1312 bp ss-DNA
ACCESSION	Sequence 1 from Patent US 4599311.
VERSION	I02706
KEYWORDS	I02706.1 GI:268359
SOURCE	.
ORGANISM	Unknown.
REFERENCE	Unknown.
AUTHORS	Unclassified.
TITLE	1 (bases 1 to 1312)
JOURNAL	Kawasaki, G. H.
FEATURES	Glycolytic promoters for regulated protein expression: protease inhibitor Patent: US 4599311-A 1 08-JUL-1986; 1547 - 16th Ave. East; Seattle, WA Location/Qualifiers

Db 1047 CCACGCCATCTTCTTCCTGCTGATGAGGGAAATACAGCACCTGGAAATGAATCA 1106
 QY 1138 CTCATGACATTTACTTAATTTTAGAGAACGAGATGCTGCTAGCGTTCTCTGACCC 1197
 Db 1107 CCCAGATATCATCAACCAAGTTCTGGAAATGAAGACAGAAAGGCTGCGCAGCTTACAT 1166
 QY 1198 TCCAAAGTTAAGTATCACCGGTACTTACGACTTAAATCTCTTTTAGGCCAGTTAGGTA 1257
 Db 1167 TACCACAACTGCTTACTTACGAACTATGATCTGAAGAGGCTCTGGTCACTGGGCA 1226
 QY 1258 TTACCAAAAGTTTCTTAAGGTCGCGATTTAGTGGTGTACTGAAGAAGCTCAATTA 1317
 Db 1227 TCACTAAGGCTCTTACGAAATGGGCTGACCTCTCCGGGTACACAGAGGACCCCTGA 1286
 QY 1318 AATTGAGTAAAGCTGTTCACAAAGCGTCTTAACATTTATGATGAAGAGGTACCGAGCG 1377
 Db 1287 AGCTCTCCNAGCGCTGATAGGCTGTGCTGACCATCGAGAGAAAGGACTGAAGCTG 1346
 QY 1378 CCGGCGCTATGTTCTTGAAGCTATTCCAATGAGCATTTCCACCAAGGTTAAATTTAATA 1437
 Db 1347 CTGGGCGCATGTTTGTAGAGGCATACCATCTCTATCCCGCGGTCAAGTTCAACA 1406
 QY 1438 ACCATTCGTTTCTGATGATGAGAGACACTAAAGGCCATTTGTTTATGGGTAAAG 1497
 Db 1407 AACCCTTTGCTCTTAAATGATGACCAAAATACCAAGTCTCCCTCTTCTATGGGAAAG 1466
 QY 1498 TTGTCAACCCAACTCAGAGTA 1519
 Db 1467 TGGTGAATCCCAACCAANAATA 1488

RESULT 7
 LOCUS AX335339 1352 bp DNA linear PAT 09-JAN-2002
 DEFINITION Sequence 5848 from Patent WO0194629.
 ACCESSION AX335339
 VERSION AX335339.1 GI:18126058
 KEYWORDS human.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
 Horridan, S., Soppet, D.R. and Weaver, Z.
 TITLE Cancer gene determination and therapeutic screening using signature
 gene sets
 JOURNAL Patent: WO 0194629-A 5848 13-DEC-2001;
 Avalon Pharmaceuticals (US)
 FEATURES Location/Qualifiers
 source 1..1352
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 349 a 386 c 325 g 292 t
 ORIGIN

Query Match 28.4%; Score 433.2; DB 6; Length 1352;
 Best Local Similarity 59.7%; Pred. No. 5.6e-83;
 Matches 729; Conservative 0; Mismatches 493; Indels 0; Gaps 0;

QY 298 TGTGTGTTAGTCTCTGTGTTTCCCACTCAAGGCCATGGAAGACCTTCAAGGGGACGCCG 357
 Db 54 TGGCAGGCTGTGCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 113
 QY 358 CTCAAAAACCGACACGATCATCAGCAAGACCATCCGACTTTTAAATAAATTAATCTC 417
 Db 114 CCCAAGACAGATATACCCACCATGATCAGGATCACCAACCTTCAACAAGATCACCC 173
 QY 418 CAATTTAGCGGAATTTGCTTTTCTTTTGTATAGACAAATAGCTCATCAAGTAATCTA 477
 Db 174 CCACTGGCTGAGTTCGGCTTTCAGCCTATACCGCAGCTGGCACACACCTCCACAGCA 233
 QY 478 CTAAATTTTTTTTAGTCCTGTTTCTATATGCCACTGCTTTTCGCCATGTTAGGTA 537

Db 234 CCAATATCTTCTTCTCCCACTGAGCATGCTACAGCCTTTGCAATGCTCTCCCTGGGA 293
 QY 538 CTAAGCGCATACCATGACGAGATTTTAGAAGGTTTAAACTTTTAAATTTGACCGAATCC 597
 Db 294 CCAAGGCTGACATCAGATGAATCTCGAGGCTGAAATTTCACTCAGGAGATTC 353
 QY 598 CAGAAGCCCAATTTACGAGGTTTCAAGAGTTTGTGAGAACTTTGAATCAACCTGAT 657
 Db 354 CGGAGGCTCAGATCCATGAAGGCTTCCAGAACTCCCTCCCTCAACCCAGACACA 413
 QY 658 CTCATTTGCAATTAACCTACTGTTAAACGTTTATTTTGTCTGAAGGTTTAAATTTGTTG 717
 Db 414 GCCAGCTCCAGCTGACCCACCGCAATGGCTGTCTCAGCAGGCGCTGAACTAGTGG 473
 QY 718 ACAATTTCTTAGAAGACGCTCAAGAAATATATATAGTAGGCTTTTACCGTTAAATTTTG 777
 Db 474 ATAGTTTGGAGGATGTTAAAGTTGTACCACTCAGAAAGGCTTCACGTGCTCACTTCG 533
 QY 778 GTGATCTGAGGAGCTTAAAGCAATTAATGATTTGTGAAAGGACCCAGGGA 837
 Db 534 GGCACACCGAAGAGGCGCAAGAAACAGATCAACGATTACGTGGAGAGGCTACTCAAGGA 593
 QY 838 AGATCGTTGACCTAGTTTAAAGAAATAGATCGTATACCGCTTTCGCACACTAGTTAACTATA 897
 Db 594 AATTTGGGATTTGGTCAAGGAGCTTGACAGAGACACAGTTTGTCTGCTGAATTTACA 653
 QY 898 TTTTTCCTCAAGGTTAAGTGGGAACGCTCTTTCGAGGTTTAAAGATACTGAAGAGGAAGATT 957
 Db 654 TCTTCTTAAGGCAATGGAGAGACCTTTTGAAGTCAAGGACACCGAGGAAGAGACT 713
 QY 958 TTCATGTTGATCAAGTTTACTTCTCAAAAGTTTCCAATGATGAAAGAGCTGGGTATGTCA 1017
 Db 714 TCCACGTGGACAGGTGACCCAGGCTGAAGTGCCTATGATGAAGCGTTTAGGCATGTTTA 773
 QY 1018 ATATTCAACATTCGAAAAAATTAAGTCTTCTGGGTCTTTATTAATGAAGTATTTAGGTAAG 1077
 Db 774 ACATCCAGCACTGTAAGAGAGCTGCCAGCTGCTGCTGATGAATAATACCTGGGCAATG 833
 QY 1078 CTACTGCTATTTTCTTTTACCAGAGCAAGGTAAGCTTCAACATTTAGAGAAATGAGTTCA 1137
 Db 834 CCACCGCATCTTCTTCTGCTGCTGATGAGGGGAAACTACAGCACTGGAAATGAATCA 893
 QY 1138 CTCATGACATTTACTTAATTTTGAAGACGAGATCGTCTGAGCGTTCTCTGACCC 1197
 Db 894 CCCACGATATCATCAACCAAGTTCTCTGGAATTAAGACAGAAAGGCTCTGCCAGCTTACATT 953
 QY 1198 TGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAATCTGTTTTCAGCCAGTAGGTA 1257
 Db 954 TACCAAACTGCTCCATTTACTGNAACCTATGATCTGAAGAGCGTCTGGGTCACTGGGCA 1013
 QY 1258 TTACCAAGTTTCTTCTAAGCGTGGCGATTTGAGTGGTGTACTGAAGAAGCTCCATTAA 1317
 Db 1014 TCACTAAGGCTCTTCAAGCAATGGGCTGACCTCTCCGGGTGACAGAGAGGACCCCTCA 1073
 QY 1318 AATTGAGTAAAGCTGTTCAAAAGCGCTCTTAACCTATTGATGAAAGGTTACCGAGCGG 1377
 Db 1074 AGCTCTCCAAAGCGCTGCAATAGGCTGTCTGACCATCGACGAGAAAGGAGTGAAGCTG 1133
 QY 1378 CCGGCGCTATGTTCTCTGGAAGCTATTTCACATGAGCATTCACCAAGGTTAAATTTAATA 1437
 Db 1134 CTGGGCGCATGTTTGTAGAGGCAATACCATGCTCTATCCCCCGGAGGTCAAGTTCAACA 1193
 QY 1438 AACCAATTCGTTTTCTGATGATCGAGCAGAACACTAAAAGCCCATTTGTTATGGTAAAG 1497
 Db 1194 AACCCCTTTGCTCTTCTTAATGATGAACAAATACCAAGTCTCCCTCTTCTATGGGAAAG 1253
 QY 1498 TTGTCAACCCAACTCAGAGTA 1519
 Db 1254 TGGTGAATCCCAACCAANAATA 1275

RESULT 8

QY 1378 CCGCGGTATGTTCTCTGGAAGCTATTCCATGAGCATTCACAGAGTTAAATTTAATA 1437
Db 1153 CTGGGGCCATGTTTATAGAGCCATCCATGCTATCCCGCCGAGGTCAAGTCAACA 1212
QY 1438 AACCATTCGTTTTCTGATGATCAGCAGAACACTAAAGCCCATTTCTTTATGGGTAAGG 1497
Db 1213 AACCTTTGCTCTTATGATGACAAATATCAAGTCTCCCTCTTCATGGGAAG 1272
QY 1498 TTGTCAACCCAACTCAGAAGTA 1519
Db 1273 TGGTGAATCCCAACCAAAATA 1294
RESULT 10
HSATPR1
LOCUS HSATPR1 1371 bp mRNA linear PRI 05-MAR-2002
DEFINITION Human mRNA for alpha 1-antitrypsin.
ACCESSION X01683
VERSION X01683.1 GI:28965
KEYWORDS antitrypsin; signal peptide.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 274)
Kurachi, K., Chandra, T., Degen, S.J., White, T.T., Marchioro, T.L.,
Woo, S.L. and Davie, E.W.
Cloning and sequence of cDNA coding for alpha 1-antitrypsin
Proc. Natl. Acad. Sci. U.S.A. 78 (11), 6826-6830 (1981)
82082539
PUBMED 7031661
TITLE 2 (bases 1 to 1371)
Bollen, A., Herzog, A., Cravador, A., Herion, P., Chuchana, P., Vander
Straten, A., Loriau, R., Jacobs, P. and van Elsen, A.
Cloning and expression in Escherichia coli of full-length
complementary DNA coding for human alpha 1-antitrypsin
DNA 2 (4), 255-264 (1983)
84107980
PUBMED 6319097
TITLE 3 (bases 1 to 1352)
Collau, B., Chuchana, P. and Bollen, A.
Revised sequence of full-length complementary DNA coding for human
alpha 1-antitrypsin
DNA 3 (4), 327-330 (1984)
85026667
PUBMED 6333329
TITLE 4
Rosenberg, S., Barr, P.J., Najarian, R.C. and Hallowell, R.A.
Synthesis in yeast of a functional oxidation-resistant mutant of
human alpha-antitrypsin
Nature 312 (5989), 77-80 (1984)
85036645
PUBMED 6387509
COMMENT Revised sequence in Colan B., Chuchana P., Bollen A.; DNA
3:327-330(1984).
FEATURES
source
1. .1371
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
39. .1295
/codon_start=1
/product="alpha 1-antitrypsin"
/protein_id="CAA25838.1"
/db_xref="GI:28965"
/db_xref="SWISS-PROT:P01009"
translation="MPSVSWGILLLAGLCLVPVSLAEDPQGDAAQKDTTSHDQDH
PTFNKTPNLAFAFSLYQLAHQSNSTNIFFSPVSIATAFAMLSLGTAKADTHDELL
GLNFLTPEAQTHEGQBELRLTNQPSQLQTLTNGNGLFSEGLKLVNDFKLEVKK
LYHSEATVNFQDEEAKQINDYVEKGTQGLVDLVKELDRDTVFALVNYIFFKGVK
ERPEVDTEEDPHVQVTVKVPMMKRLGMENIOHCKLSWMLKVLGNATIF
FLPDEGLQHLNELTHDILITKPLENEDRSASLHLPKLSITGTDLKSVLGGLITK
VFSNGADLSGVTEERAPLKLKSAVHKAVLITDEKGTGAAGNFLEAIPMSIPPEVKENK

PFVFLMIQNTKSPLEFMGVVNPQK*
39. .110
mat_peptide 111. .1292
/product="unnamed"
polya_site 1371
BASE COUNT 350 a 388 c 340 g 293 t
ORIGIN
Query Match 28.4%; Score 433.2; DB 9; Length 1371;
Best Local Similarity 59.7%; Pred. No. 5.5e-83;
Matches 729; Conservative 0; Mismatches 493; Indels 0; Gaps 0;
QY 298 TGTGTGTAAGTCTGTGTTTCCCGAGTCAAGGCGCATGAAGACCTCAAGGCGAGCGG 357
Db 73 TGGCAGCGCTGTGCTGCCCTGCTGCTCCCTGGCTGAGGATCCCGAGGAGATGCTG 132
QY 358 CTCAAAAAACCCGACACAGTCATCAGCACCAGACCATCCGACTTTTAAATAAAATTAATC 417
Db 133 CCAGAGACAGATACATCCACCATGATCAGGATCACCACACCTTCAACAAGATCACCC 192
QY 418 CAAATTTAGCGAATTTGCTTTTCTTGTATAGACAATAGCTCATCAAGTAATTTCTA 477
Db 193 CCAACCTGGCTGAGTTTCGCTTACGCTATACCGCAGCTGGCACACCATCCACAGCA 252
QY 478 CTAAACATTTTCTAGTCTGCTTCTATTGCGCAGTCTGCTTCCGCTGTTGAGTTTAGGTA 537
Db 253 CCAATATCTTCTTCTCCCGAGTGAATCGCTACAGCTTTCGATGCTCTCCCTGGGA 312
QY 538 CTAAAGCCGATACCCATGACGAGATTTTGAAGGTTTAAACTTTAATTTGACGAAATCC 597
Db 313 CCAAGGCTGACACTCAGCATGAATCCTGGAGGCTGAATTTCAACCTCAGGAGATTC 372
QY 598 CAGAGCCCAATTCAGAGGGTTTCAAGAGTTGTTGAGAACTTTGAGAACTTTGAATCAACCTGAT 657
Db 373 CGGAGGCTCAGATCCATGAAGGCTTCCAGGAACTCTCTCCCTCAACCCAGCAGACA 432
QY 658 CTCAATTCGAATTAAGTCTGTTAAGGTTTATTTTGTCTGAAGGTTTAAATTTGGTTG 717
Db 433 GCCAGCTCCAGCTGACCCAGCAATGGCTGTTCTCAGCAGGAGGCTTGAAGTAGTGG 492
QY 718 ACAATTCCTAGAGAGCTCAAGAACTATATCATAGTAGGCTTTACCGTTAATTTTG 777
Db 493 ATAAGTTTGGAGGATGTTAAAGTTGTACCACCTCAGAAAGCTTCACTGTCAACTGG 552
QY 778 GTGATCTAGGAAGCTAAAGCAAAATTAAGTATGTTTGAAGAAGCAGCCAGGCTA 837
Db 553 GGCACACCGAAGAGCGCAAGAAACAGATCAACGATTAACGTTACGTGGAGAGGGTACTCAAGGA 612
QY 838 AGATCGTTGACCTAGTTTAAAGAAATTAAGTCTGATACCGTCTTCGCACCTAGTTAACTATA 897
Db 613 AAATTTGGGATTTGGTCAAGGAGCTTGCAGAGACAGATTTTGTCTCTGGTGAATTA 672
QY 898 TTTTTCCTCAAGGTAAGTGGGAGCTCTTTCGAGGTTAAAGATACCTGAAGAGGAAT 957
Db 673 TCCTTTTAAAGCAATGGGAGAGCTTTCGAAGTCAAGGAGACCCGAGGAGAGGACT 732
QY 958 TCCATGTTGATCAAGTTTACTTCTCAAGTTCCTCAATGATGAAGAACTGGGTATGTTCA 1017
Db 733 TCCACGTGGACAGGTGACCCAGCTGAAAGTGCCTATGATGAAGCGCTTTAGCATGTTTA 792
QY 1018 ATATTCAACATTCGAAAAAATTAAGTTCTTGGCTCTTATTAAATGAAGTATTAGGTAAGC 1077
Db 793 ACATCAGCACTGTAAAGAGCTGTCCAGCTGGGTGCTGCTGATGAATACCTGGGCAATG 852
QY 1078 CTACTGCTATTTTCTTCTCCCTGATGAGGGGAACTACAGCACCTGGAAAAATGAATCA 912
Db 853 CCACCGCATCTTCTTCTCCCTGATGAGGGGAACTACAGCACCTGGAAAAATGAATCA 912
QY 1138 CTCATGACATTTACTAAATTTTATAGAGAACAGGATCGTCGTAGCGCTTCTCTGACC 1197
Db 913 CCCACGATATCATCAACAGTCTCTGAAAAATGAAGACAGAGGCTCTGCCAGCTTACAT 972
QY 1198 TGCAAAAGTTAAGTATACCCGGTACTTACGACTTAAAACTGTGTTTAGGCCAGTTAGGTA 1257

QY 898 TTTTTCAGGTAAGTGGGAACGTCCTTTTCGAGGTTAAAGATACTGAAGAGAGATT 957
 Db 681 TCCTTCCTTAAAGCAATGGGAGACCTTTGAAGTCAAGGACACCCGAGGAGGACT 740
 QY 958 TTCAATGTTGATCAAGTTACTACGTCAAAAGTTCCAAATGATGAAAAGACTGGGTATGTTCA 1017
 Db 741 TCCACGTGGACCAAGTGACCAAGTGAAGTGCCTATGATGAAGCGTTTAGGCATGTTTA 800
 QY 1018 ATATTCAACATTCGAAAAATTAAGTTCCTGGGTCTTATTAATGAAGTATTAGGTACG 1077
 Db 801 ACATCCAGCACTTAAGAAGCTGTCAGGTGGGTGCTGCTGATGAATACCTGGCAATG 860
 QY 1078 CTACTGCTATTTTTCACAGACGAAGTTCAAGCTTCAACATTTAGAGAAATGAGTTGA 1137
 Db 861 CCACCCCATCTTCCTCCCTGATGAGGGGAACTACAGCACCTGGAAATGAACCTCA 920
 QY 1138 CTATGACATTAATTAATAATTTTATAGAACGAGGATCGTGTAGCGCTTCTCTGCACC 1197
 Db 921 CCCACGATATCATCACAAGTTCCTGGAAAAATGAAGACAGAAGGTCTGCCAGCTTACATT 980
 QY 1198 TGCCTAAGTTAAGTATACCCGCTACTTACGACTTAAATCTGTTTTAGGCCAGTTAGGTA 1257
 Db 981 TACCCAAACTGTCCANTTACTGGAACCTATGATCTGAAGAGCGCTCTGGGTCAACTGGGCA 1040
 QY 1258 TTACCAAAAGTTTTCCTAAGCGTGGCGATTGAGTGGTGTACTGAAGAAGCTCCATTAA 1317
 Db 1041 TCACTAAGGTCTTCAGCAATGGGGCTGACCTTCCGGGGTCACAGAGAGGACCCCTGA 1100
 QY 1318 AATTGAGTAAAGCTGTTCAAAAGCGCTCTTAACATTTGATGAAAAGGTACCGAGGCG 1377
 Db 1101 AGCTCTCCAAGGCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAGGACTGAGCTG 1160
 QY 1378 CCGGGCGTATGTTCCCTGGGAGCTATTCCAATGAGCATTCACCCAGAAAGTTAATTAATA 1437
 Db 1161 CTGGGGCCATGTTTTAGAGGCCATACCCATGTCTATCCCCCGAGGTCAAGTTCACACA 1220
 QY 1438 AAGCATTCGTTTTCTCTGATGATCGAGCAGAACACTAAAGCCCATTTGTTATGGGTAAGG 1497
 Db 1221 AACCTTTGCTCTTAAATGATTGAACAAAATACCAAGTCTCCCTCTTCATGGGAAAG 1280
 QY 1498 TTGTCACCCCACTCAGAAGTA 1519
 Db 1281 TGCTGAATCCCAAAAAATA 1302

Search completed: December 7, 2002, 01:14:50
 Job time : 2703.5 secs

